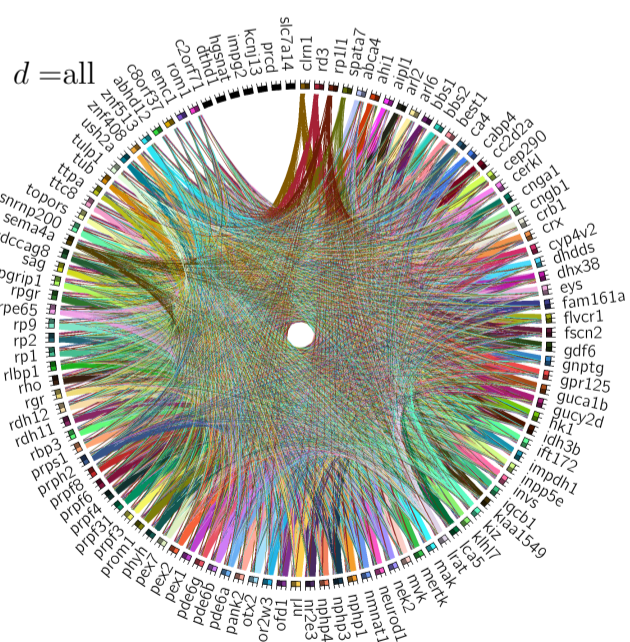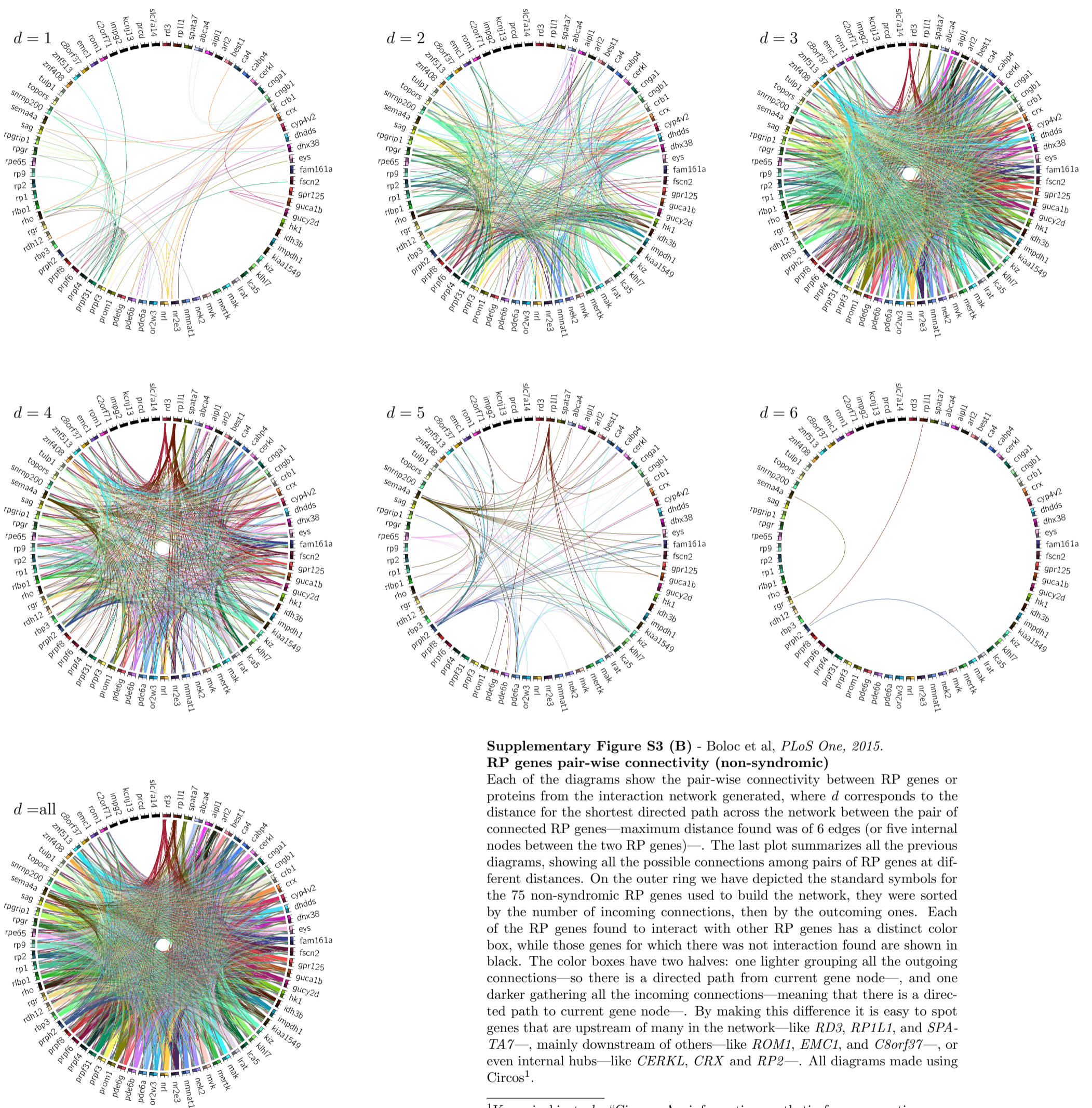**Supplementary Figure S3 (A)** - Boloc et al, *PLoS One, 2015.*
RP genes pair-wise connectivity (all)
Each of the diagrams show the pair-wise connectivity between RP genes or
proteins from the interaction network generated, where d corresponds to the
distance for the shortest directed path across the network between the pair of
connected RP genes—maximum distance found was of 6 edges (or five internal
nodes between the two RP genes)—. The last plot summarizes all the previous
diagrams, showing all the possible connections among pairs of RP genes at dif-
ferent distances. On the outer ring we have depicted the standard symbols for
the 110 RP/ genes used to build the network, they were sorted by the number
of incoming connections, then by the outcoming ones. Each of the RP genes
found to interact with other RP genes has a distinct color box, while those
genes for which there was not interaction found are shown in black. The color
boxes have two halves: one lighter grouping all the outgoing connections—so
there is a directed path from current gene node—, and one darker gathering all
the incoming connections—meaning that there is a directed path to current ge-
ne node—. By making this difference it is easy to spot genes that are upstream
of many in the network—like *CLRN1*, *RD3*, *RP1L1*, and *SPATA7*—, mainly
downstream of others—like *ABHD12*, *ROM1*, *EMC1*, and *C8orf37*—, or even
internal hubs—like *PEX1*, *IQCB1*, *CERKL*, *CRX* and *RP2*—. All diagrams
made using Circos[1].

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[1]Krzywinski *et al.* "Circos: An information aesthetic for comparative geno-
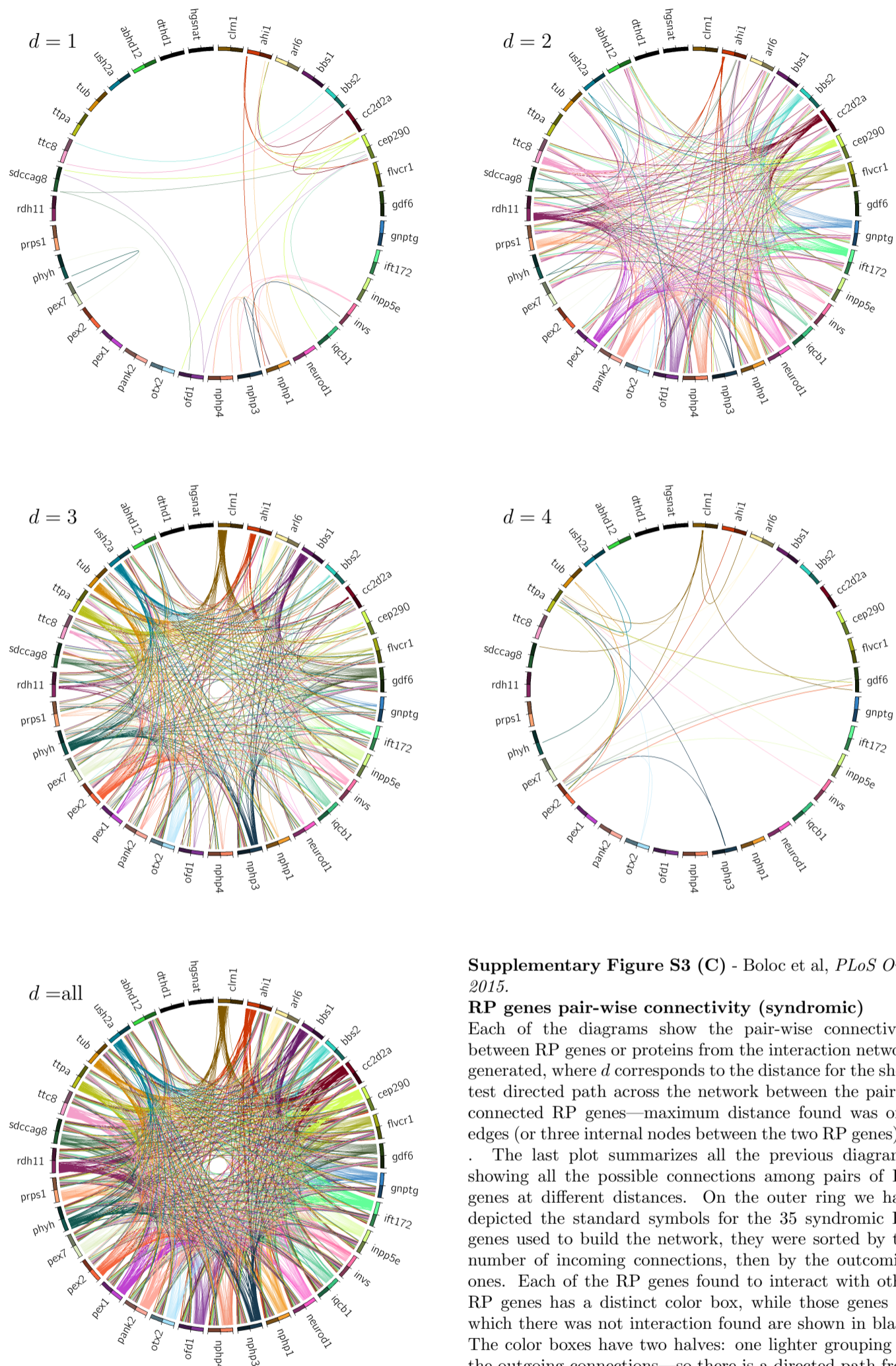mics." *Genome Research*, 19(9):1639–1645, 2009.

Supplementary Figure S3 (B) - Boloc et al, *PLoS One, 2015*.
RP genes pair-wise connectivity (non-syndromic)

Each of the diagrams show the pair-wise connectivity between RP genes or proteins from the interaction network generated, where d corresponds to the distance for the shortest directed path across the network between the pair of connected RP genes—maximum distance found was of 6 edges (or five internal nodes between the two RP genes)—. The last plot summarizes all the previous diagrams, showing all the possible connections among pairs of RP genes at different distances. On the outer ring we have depicted the standard symbols for the 75 non-syndromic RP genes used to build the network, they were sorted by the number of incoming connections, then by the outcoming ones. Each of the RP genes found to interact with other RP genes has a distinct color box, while those genes for which there was not interaction found are shown in black. The color boxes have two halves: one lighter grouping all the outgoing connections—so there is a directed path from current gene node—, and one darker gathering all the incoming connections—meaning that there is a directed path to current gene node—. By making this difference it is easy to spot genes that are upstream of many in the network—like *RD3*, *RP1L1*, and *SPATA7*—, mainly downstream of others—like *ROM1*, *EMC1*, and *C8orf37*—, or even internal hubs—like *CERKL*, *CRX* and *RP2*—. All diagrams made using Circos[1].

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[1]Krzywinski *et al.* "Circos: An information aesthetic for comparative genomics." *Genome Research*, 19(9):1639–1645, 2009.

RP genes pair-wise connectivity (syndromic)

Each of the diagrams show the pair-wise connectivity between RP genes or proteins from the interaction network generated, where d corresponds to the distance for the shortest directed path across the network between the pair of connected RP genes—maximum distance found was of 4 edges (or three internal nodes between the two RP genes)—. The last plot summarizes all the previous diagrams, showing all the possible connections among pairs of RP genes at different distances. On the outer ring we have depicted the standard symbols for the 35 syndromic RP genes used to build the network, they were sorted by the number of incoming connections, then by the outcoming ones. Each of the RP genes found to interact with other RP genes has a distinct color box, while those genes for which there was not interaction found are shown in black. The color boxes have two halves: one lighter grouping all the outgoing connections—so there is a directed path from current gene node—, and one darker gathering all the incoming connections—meaning that there is a directed path to current gene node—. By making this difference it is easy to spot genes that are upstream of many in the network—like *CLRN1*—, mainly downstream of others—like *ABHD12*—, or even internal hubs—like *PEX1* or *IQCB1*—. All diagrams made using Circos[1].

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[1] Krzywinski *et al.* "Circos: An information aesthetic for comparative genomics." *Genome Research*, 19(9):1639–1645, 2009.